Listing of claims:

Claim 1 (amended): A method of detecting at least first and second target molecules in a sample comprising:

~~a.~~ a)contacting said first and second target molecule with a composition comprising:

~~i.~~ i) an amplification enzyme; and

~~ii.~~ ii) first and second target probes, said first and second target probes comprising:

(a) a first and a second bioactive agent, respectively, wherein said first and second bioactive agents specifically bind to said first and second target molecules, respectively;

(b) a first and a second adapter sequence, respectively, wherein said first adapter sequence identifies said first target molecule and said second adapter sequence identifies said second target molecule; and

(c) at least a first and a second upstream universal priming sequences;

~~b.~~ b) amplifying said first and second adapter sequences using said first and second universal priming sequences, wherein no ligation is performed, to form first and second amplicons, respectively;

~~c.~~ c) detecting said first and second amplicons, respectively, to indicate the presence [or absence] of said first and second target molecules in said sample.

Claim 2 (original) The method according to claim 1, wherein said first and second target molecules are selected from the group consisting of proteins and nucleic acids.

Claims 3-10 (withdrawn)

Claim 11 (original): The method according to claim 2, wherein said first and second target molecules are proteins.

Claims 12-13 (withdrawn):

Claim 14 (original): The method according to claim 11, wherein at least said first bioactive agent is an aptamer.

Claim 15 (original): The method according to claim 11, wherein said first and second upstream universal priming sequences are RNA Polymerase primers and said enzyme is an RNA Polymerase.

Claim 16 (original): The method according to claim 15, wherein said first and second upstream universal priming sequences are T7 RNA Polymerase primers.

Claim 17 (amended): The method according to claim 11, further comprising contacting said first and second upstream universal priming sequences with first and second chimeric

RNA/DNA primers, respectively, ~~wherein said amplification is by SPIA~~ prior to said amplifying.

Claim 18 (original): The method according to claim 11, wherein said first and second target probes further comprise first and second downstream universal priming sequences, wherein said first and second upstream universal priming sequences and said first and second downstream universal priming sequences flank said first and second adapter sequences, respectively.

Claim 19 (original): The method according to claim 1, wherein said composition further comprises nucleotides.

Claim 20 (original): The method according to claim 19, wherein at least said nucleotides are labeled nucleotides.

Claim 21 (amended): The method according to claim 1, wherein said detecting comprises:

~~a.~~ a) contacting said first and second amplicons with at least one substrate comprising first and second capture probes, wherein said first capture probes are complementary to said first adapters and said second capture probes are complementary to said second adapters; and

~~b.~~ b) detecting said first and second amplicons on said at least one substrate.

Claims 22-23 (withdrawn)

Claim 24 (original): The method according to claim 21, wherein said substrate comprises at least a first and a second population of microspheres, wherein said first capture probes are immobilized on said first population of microspheres and said second capture probes are immobilized on said second population of microspheres.

Claim 25 (original): The method according to claim 24, wherein said first and second amplicons are detected in a liquid array.

Claim 26 (original): The method according to claim 25, wherein said first and second amplicons are detected by FACS.

Claim 27 (original): The method according to claim 24, wherein said microspheres are randomly distributed on a second substrate comprising discrete sites.

Claim 28 (original): The method according to claim 24, wherein said microspheres are applied to a mass spectrometer and the mass of said adapter sequence is determined to identify the presence of said first and second target molecules.

Claim 29 (amended): A method for multiplex detection of a plurality of target molecules in a sample said method comprising;

~~a.~~ a) contacting said plurality of target molecules with a composition comprising~~:~~

~~i. an amplification enzyme; and~~

~~ii.~~ a plurality of target probes, each comprising:

~~a)~~ i) a bioactive agent, wherein each bioactive agent binds to a unique target molecule;

~~b)~~ ii) an adapter sequence that identifies said unique target molecule that binds the bioactive agent; and

~~c)~~ iii)at least one upstream universal priming sequence;

b) removing unbound target probes, leaving bound target probes;

c) contacting said bound target probes with an amplification enzyme;

[b.] d) amplifying said adapter sequences of said bound target probes using said at least one universal priming sequence, wherein no ligation is performed, to form a plurality of amplicons;

[c.] e) detecting said plurality of amplicons, to indicate the presence or absence of said target molecules in said sample.

Claim 30 (original): The method according to claim 29, wherein said target molecules are selected from the group consisting of proteins and nucleic acids.

Claim 31 (original): The method according to claim 30, wherein said target molecules are proteins.

Claim 32. (withdrawn)

Claim 33. (previously amended) The method according to claim 29 or 30, wherein said plurality of target molecules comprises at least 500 target molecules.

Claim 34. (withdrawn)